A persistent antimicrobial resistance pattern and limited methicillin-resistance-associated genotype in a short-term Staphylococcus aureus carriage isolated from a student population

ABSTRACT

The aim of the present study was to assess and compare the antimicrobial susceptibility pattern against a panel of antibiotics and molecular and methicillin resistance-associated genotypes of 120 carriage S. aureus isolates previously isolated from a student population at two isolation events within a one-month interval. The antibiotic susceptibility of isolates was determined using the Kirby-Bauer disc-diffusion method (cefoxitin by Etest). The MRSA was screened using polymerase chain reaction for the presence of the mecA gene. The mecA-positive isolates were subjected to staphylococcal cassette chromosome (SCC) mec typing, multilocus sequence typing (MLST) and eBURST analysis. All isolates were characterized for the presence of the Pantonï Valentine leukocidin (PVL) gene, an enterobacterial repetitive intergenic consensus-polymerase chain reaction (ERIC-PCR) pattern and the spa type. For the two occasions where S. aureus was isolated, the highest frequency of resistance was observed for penicillin (70% and 65%, respectively), with a lower rate against erythromycin and tetracycline (<12%). All isolates were susceptible to ciprofloxacin and gentamycin. As for methicillin resistance, eight isolates had minimum inhibitory concentrations (MIC) of resistant categories, but 10 isolates (8.33%) were positive for the mecA gene. The mecA-positive isolates belonged to SCCmec types I (n = 9) and V (n = 1). MLST was resolved for only three MRSAs, ST508 (n = 1), ST88 (n = 1) and ST96 (n = 1). The results of the eBURST analysis showed that the MRSA isolates analyzed in the present study were potentially related to MRSA identified in other countries. Approximately half of the persistent S. aureus carriers harbored S. aureus of a similar spa type in the respective individuals during both isolation events. A persistent antimicrobial pattern and limited distinct MRSAs were observed over the short study period. The latter frequently exhibited SCCmec type I, commonly associated with hospital-acquired (HA) characteristics, but further delineation is needed to justify the origins of these bacteria.

Keyword: Antimicrobial; MRSA; Staphylococcus aureus; mecA gene